

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:08:31 ; Search time 17398.4 seconds
(without alignments)
695.856 Million cell updates/sec

Title: US-09-303-518D-569

Perfect score: 897

Sequence: 1 atgttcgttaccatcag.....accgcacaacatgcgtaa 897

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vitc:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40.4	4.5	1101	12 CNSO0KR2	AL077673 Drosophila
2	40	4.5	1009	10 BG701305	BG701305 602682983
3	38	4.2	703	10 B1917026	B1917026 603181414
4	38	4.2	1101	9 AL513871	AL513871 AL513871
5	37.6	4.2	1592	10 BM451350	BM451350 AGENCOURT
6	37.4	4.2	1815	11 AK014308	AK014308 Mus muscu
7	37.2	4.1	972	12 CNSO02JV	AK014308 Mus muscu
8	37	4.1	656	9 AV402539	AL097765 Drosophila
9	37	4.1	732	9 AV006052	AV402539 AV402539
10	37	4.1	928	9 AU006052	AU006052 AU006052
11	37	4.1	1013	12 BE214094	BE214094 HY-CEB000
12	36.4	4.1	884	12 CNSO16KT	AL066871 Drosophila
13	36.2	4.0	643	9 BB620231	BB620231 BB620231
14	36.2	4.0	643	9 BB657008	BB657008 BB657008
15	36.2	4.0	653	10 BM491204	BM491204 PGP2n-PK0
16	36.2	4.0	685	9 BB645508	BB645508 BB645508
17	36.2	4.0	1012	10 BG115639	BG115639 602316767

C	18	36	4.0	614	12 AQ082014	AQ082014 RPI11-54
C	19	36	4.0	686	10 BG107224	BG107224 602290957
C	20	36	4.0	970	10 BM461835	BM461835 AGENCOURT
C	21	36	4.0	1243	10 BM460646	BM460646 AGENCOURT
C	22	36	4.0	1247	10 BM466205	BM466205 AGENCOURT
C	23	35.8	4.0	343	9 AV673531	AV673531 AV673531
C	24	35.8	4.0	430	10 BG047727	BG047727 CVL-27-A1
C	25	35.8	4.0	507	10 BE599418	BE599418 P11-87-C1
C	26	35.8	4.0	608	9 AV902676	AV902676 AV902676
C	27	35.8	4.0	914	12 CNSO06CP	AL059740 Drosophila
C	28	35.8	4.0	1201	12 BE65323	BE65323 Drosophila
C	29	35.8	4.0	1590	10 BE95996	BE95996 601659233
C	30	35.6	4.0	563	10 AL551924	AL551924 484611 MA
C	31	35.6	4.0	880	9 AL1933541	AL1933541 w40c01.x
C	32	35.4	3.9	330	9 BF622032	BF622032 HVSME1000
C	33	35.4	3.9	695	10 BF079098	BF079098 229628 MA
C	34	35.2	3.9	568	10 AL502466	AL502466 AV931238
C	35	35.2	3.9	700	9 AV931238	AV931238 AV931238
C	36	35	3.9	600	9 BM486648	BM486648 PGM2n-PK0
C	37	35	3.9	618	10 AV926352	AV926352 AV926352
C	38	35	3.9	645	9 BM047100	BM047100 603627433
C	39	35	3.9	822	10 AV869097	AV869097 AV869097
C	40	35	3.9	894	10 AL514205	AL514205 AL514205
C	41	34.8	3.9	516	9 AL530594	AL530594 AL530594
C	42	34.8	3.9	565	9 AM659434	AM659434 96602 MAR
C	43	34.8	3.9	840	9 AM922863	AM922863 DGL-47.H1
C	44	34.6	3.9	530	10 BG560454	BG560454 RH122-74
C	45	34.6	3.9	548	9 AM054381	AM054381 L30-17192
C	46	34.6	3.9	707	10 BH132869	BH132869 ENTO185TF
C	47	34.6	3.9	869	12 CNSO06CN	AL063629 Drosophila
C	48	34.6	3.9	910	12 CNSO17SY	AL104440 Drosophila
C	49	34.6	3.9	1101	12 CNSO14PA	C06823 C06823 Rat
C	50	34.6	3.9	1101	12 C06823	AL161299 Leishmani
C	51	34.4	3.8	482	12 AQ491449	AQ491449 RPI1-11-2
C	52	34.4	3.8	513	12 CNSO04NB	AL054280 Drosophila
C	53	34.4	3.8	559	12 CNSO17SY	AL054280 Drosophila
C	54	34.4	3.8	839	12 CNSO17SY	AL054280 Drosophila
C	55	34.2	3.8	1101	12 CNSO17SY	AL054280 Drosophila
C	56	34.2	3.8	627	9 A1825645	A1825645 w75b05.x
C	57	34.2	3.8	629	9 AV872025	AV872025 AV872025
C	58	34.2	3.8	730	9 BB645299	BB645299 BB645299
C	59	34.2	3.8	909	12 CNSO0JTL	AL076720 Drosophila
C	60	34.2	3.8	1100	12 CNSO16KD	AL106855 Drosophila
C	61	34.2	3.8	407	10 BF039324	BF039324 BP25009A
C	62	34	3.8	491	10 BE776714	BE776714 MY-19-E-0
C	63	34	3.8	588	9 AL652306	AL652306 AL652306
C	64	34	3.8	612	9 AM587084	AM587084 EST18707
C	65	34	3.8	658	12 AQ397507	AQ397507 m9xb0009J
C	66	34	3.8	765	10 BG584885	BG584885 EST486646
C	67	34	3.8	802	10 BE368219	BE368219 60122141
C	68	34	3.8	1194	10 BG820654	BG820654 602782958
C	69	33.8	3.8	425	12 AZ048716	AZ048716 GSSBR010
C	70	33.8	3.8	455	10 BE773885	BE773885 283396 MA
C	71	33.8	3.8	455	10 W07842	W07842 zB04B03.r1
C	72	33.8	3.8	478	10 BM286331	BM286331 526343 MA
C	73	33.8	3.8	480	10 BM258834	BM258834 523748 MA
C	74	33.8	3.8	508	10 BM114584	BM114584 LO807B07-
C	75	33.8	3.8	525	9 AM9229511	AM9229511 EST338299
C	76	33.8	3.8	645	12 CNSO1213	AL101589 Drosophila
C	77	33.8	3.8	727	12 B1805731	B1805731 S043412.S
C	78	33.8	3.8	895	12 CNSO071A	AL066286 Drosophila
C	79	33.6	3.7	287	9 AV131659	AV131659 AV131659
C	80	33.6	3.7	360	10 C42003	C42003 C42003 Yuj1
C	81	33.6	3.7	367	10 B1720178	B1720178 1031048B0
C	82	33.6	3.7	471	9 AV624652	AV624652 AV624652
C	83	33.6	3.7	487	9 A1336998	AL1336998 qx87e10.x
C	84	33.6	3.7	487	10 B1183298	B1183298 UNL-P-FN-
C	85	33.6	3.7	489	10 B1186294	B1186294 UNL-P-FN-
C	86	33.6	3.7	498	9 AM594194	AM594194 h962a01.x
C	87	33.6	3.7	517	10 B1874475	B1874475 963115H01
C	88	33.6	3.7	546	9 AM237064	AM237064 xms2902.x
C	89	33.6	3.7	551	9 A1989498	A1989498 ws25e01.x
C	90	33.6	3.7	588	10 BE463918	BE463918 hy18h06.x

c	91	33.6	3.7	601	10	B1718274	B1718274	1031030FO
	92	33.6	3.7	643	10	BMA40578	BMA40578	pgr1L-PK0
	93	33.6	3.7	725	10	B1517775	B1517775	603042019
c	94	33.6	3.7	735	10	B1993866	B1993866	1031005B0
c	95	33.6	3.7	786	10	BG845957	BG845957	1024011C0
c	96	33.6	3.7	832	9	AL534397	AL534397	AL534397
c	97	33.6	3.7	893	9	AL521848	AL521848	AL521848
c	98	33.6	3.7	937	9	AL534844	AL534844	AL534844
	99	33.6	3.7	968	10	B1225970	B1225970	602955048
	100	33.6	3.7	1101	12	CNS0150D	AL104839	Drosophila

ALIGNMENTS

[illegible]

Qy	588	cctgcgccaccacgctccccctccctcaagaag	619
		::: ::::: ::::: ::: ::	
Db	1067	AGKKKKKMMVMMMKKMMMVNDGKMMMAKMAADK	1098

LOCUS	DEFINITION	1101 bp	DNA	linear	GSS_03-JUN-1999
CNS00KR2	CNS00KR2				
LOCUS	Drosophila melanogaster genome survey sequence T7 end of BAC:				
DEFINITION	BACR17F2.2 of RP11-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.				

ACCESSION	AL077673	GI:4957249
VERSION	AL077673.1	
KEYWORDS	GSS.	
SOURCE	fruit fly.	
ORGANISM	Drosophila melanogaster	

REFERENCE
1 (phases 1 to 1101)

REFERENCE
1 (bases 1 to 1101)
AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage :
direct submission - genome / E-mail : secreff@genoscope.cns.fr
no stat analysis - genome / E-mail : secreff@genoscope.cns.fr

COMMENT

Determination of this BAC-end sequence was carried out as part of a project funded by the French Government (Genome Project (ANGP))

- Web : www.genoscope.cns.fr

BR 191 51006 EVRI CEDEX 2 FRANCE (2 mail : regis@genoscope.cns.fr)

collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see http://www.fruitfly.org/TheBDGP/Drosophila_melanogaster_BAC_library was prepared by Kazutoyo Oosagawa and Aaron Mammaster in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPci-98 and was constructed by partial EcoRI digestion of *Drosophila* DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's 101 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

```

FEATURES
source      Location/Qualifiers
1. .1101

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/organism="Drosophila melanogaster"  
/db_xref="taxon:7227"  
/clone_lib="RPCI-98"  
/clone="BACR17F22"
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BASE COUNT	191 a	94 c	163 g	151 t	502 others
ORIGIN					

Query Match	4.5%;	Score 40.4;	DB 12;	length 1101;
Best Local Similarity	9.6%;	Pred. No. 2.5;		
Matches 32;	Conservative 159;	Mismatches 141;	Indels 0;	Gaps 0

OY

288 agcagatagaacaacatgttcgaagcggttacacgycgtgtaaacatctgcagcaaggctttggaa	34
: :: :	:::: :
: :: :: :	:::: :

Db 767 AKAGMAMMAAMAMAKEDNAKAMMMMMGMMMMVAKMGIMSGMGKHMGRKMGITIM 828

348 caaacacgaagcgctgcatactcatcagccgcacatcgcgacgtacgatttggcgcagc 407

Db 827 MRKNV NKMGMAK NKMBBAMMMMMK MNKD KMNMC KIKCNMKMK YMMMMMA KM 88

RESULT	2
BG701305/c	
BG701305	1009 bp
LOCUS	mRNA
60268283r31	linear
DEFINITION	EST 07-MAY-2001
NH_MGC_95	Homo sapiens CDNA clone IMAGE:4815380 5',
mrna sequence.	

ACCESSION	EG701305	
VERSION	BG701305.1	GI:13971506
KEYWORDS	Est.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1009)
Enkariaota, Metazoa; Chordata; Cnaniata;Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Carnarihihi; Homnidae; Homo.
Nih-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Tissue procurement: Miklos Palkovits, M.D., Ph.D.
cDNA library preparation: Michael J. Brownstein (NHGRI), Shirak
Toshiyuki and Piero Carninci (RIKEN)
cDNA library arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LLAM0712 row: f column: 21
high quality sequence stop: 121

FEATURES
source

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    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="IMAGE:4815380"
    /clone_1ib="NIH_MGC_95"
    /tissue_type="hippocampus"
    /ab_bestsituation

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BASE COUNT	245 a	243 c	260 g	260 t	1 olive/s
ORIGIN					

Query Match	4.5%	Score 40;	DB 10;	Length 1009;
Best local Similarity	57.08;	Pred. No. 3.2;		
Matches 73; Conservative	0;	Mismatches 55;	Indels 0;	Gaps 0.

DY 549 aaatcatcaagccctgctgcgtcggaagaacactcgttctgccgacgaagtcccctc 608
||||| ||| ||||| | | | | | | | | | | | |
Db 137 AATCAGCAATGCGCTGGGCCAGCTACGCTCCCGCATTCACGGCGCACACAAGCACCATC 78

Db	Accession	Source	Organism	Accession	Source	Organism
01	AB000001	GenBank	Human	AB000001	GenBank	Human
02	AB000002	GenBank	Human	AB000002	GenBank	Human
03	AB000003	GenBank	Human	AB000003	GenBank	Human
04	AB000004	GenBank	Human	AB000004	GenBank	Human
05	AB000005	GenBank	Human	AB000005	GenBank	Human
06	AB000006	GenBank	Human	AB000006	GenBank	Human
07	AB000007	GenBank	Human	AB000007	GenBank	Human
08	AB000008	GenBank	Human	AB000008	GenBank	Human
09	AB000009	GenBank	Human	AB000009	GenBank	Human
10	AB000010	GenBank	Human	AB000010	GenBank	Human
11	AB000011	GenBank	Human	AB000011	GenBank	Human
12	AB000012	GenBank	Human	AB000012	GenBank	Human
13	AB000013	GenBank	Human	AB000013	GenBank	Human
14	AB000014	GenBank	Human	AB000014	GenBank	Human
15	AB000015	GenBank	Human	AB000015	GenBank	Human
16	AB000016	GenBank	Human	AB000016	GenBank	Human
17	AB000017	GenBank	Human	AB000017	GenBank	Human
18	AB000018	GenBank	Human	AB000018	GenBank	Human
19	AB000019	GenBank	Human	AB000019	GenBank	Human
20	AB000020	GenBank	Human	AB000020	GenBank	Human
21	AB000021	GenBank	Human	AB000021	GenBank	Human
22	AB000022	GenBank	Human	AB000022	GenBank	Human
23	AB000023	GenBank	Human	AB000023	GenBank	Human
24	AB000024	GenBank	Human	AB000024	GenBank	Human
25	AB000025	GenBank	Human	AB000025	GenBank	Human
26	AB000026	GenBank	Human	AB000026	GenBank	Human
27	AB000027	GenBank	Human	AB000027	GenBank	Human
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37	AB000037	GenBank	Human	AB000037	GenBank	Human
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41	AB000041	GenBank	Human	AB000041	GenBank	Human
42	AB000042	GenBank	Human	AB000042	GenBank	Human
43	AB000043	GenBank	Human	AB000043	GenBank	Human
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47	AB000047	GenBank	Human	AB000047	GenBank	Human
48	AB000048	GenBank	Human	AB000048	GenBank	Human
49	AB000049	GenBank	Human	AB000049	GenBank	Human
50	AB000050	GenBank	Human	AB000050	GenBank	Human

TITLE	JOURNAL	COMMENT	FEATURES
D.W., Fenton,R.D., Oates,R. and Main,D. Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mia6) seedling leaf cDNA library	Unpublished (2001)	Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: twing@clemson.edu Total hg bases = 450 Seq primer: AATTACCTGACTAAGGC High quality sequence stop: 570.	Source 1. .928 /organism="Hordeum vulgare" /cultivar="C116151 (Mia6)" /db.xref="taxon:4513" /clone="HV_CED0002D12f" /clone_id="Hordeum vulgare seedling green leaf EST library HVCDNA0005 (Blumeria challenged)" /tissue_type="seedling green leaf" /lab_host="SOLR" /note="Vector: lambdaZAP; Site:1: EcoRI; Site:2: XhoI; C.I. 16151 (Mia6) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate 5874 (AvrMia6) of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wel, Wise). In the T1 close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantites of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley . To order this clone see http://www.genome.clemson.edu/orders Also see Close JY, Wing R, Kleinof A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley genomics Newsletter 31:29-30. (http://wheat.pw.usda.gov/g9pages/D9n/31/cover.html)"
BASE COUNT	159 a	319 c	308 g
ORIGIN	138 t	4 others	
Query Match	4.1%;	Score 37;	DB 9;
Best Local Similarity	56.0%;	Pred. No. 21;	Length 928;
Matches	70;	Conservative	0;
		Mismatches	55;
		Indels	0;
		Gaps	0;
QY	333	gcagcagcgtttggaacaaacgaagagcgctgcattcatcaccgacacatcgagcagcta	392
DB	249	gctggcgcccccagagacacacagagggcgaggttcacatttgcgccttgagacgcgcgactccc	308
QY	393	cgattttggcgcgcgtacatcagcagcagcagccttcctccgcgtcagcgcagcgtatcagta	452
DB	309	ggccatctcttggcgcgtatctccacgcagagcccttggccatctcctgcctccatgcagcat	368
QY	453	accgcg	457
DB	369	ggcgcg	373

OY 144 cctttaagggaagaagccgagcgagcaltcgtgccaatatgctgaagcagcagtaatcc 203
 Db 718 ACTTGAGATGGGGTTCCTCCGCGCCGACGATAGACAGACGATCAGTGGAAAGAACCCGCTTC 777
 OY 204 CGAGCCCCAAGCGTCAAGCGCTTTTtgcgga 236
 Db 778 GGTCAAAAACGGGCGCGACGCTCTCTTAAGGA 810

RESULT	18
A0082014/c	
LOCUS	
DEFINITION	614 bp DNA linear
ACCESION	NC_009820.1
	RPcII1-54G19, TJ RPcI-11 Homo sapiens genomic clone RPcI-11-54G19, DNA sequence.

Clones are derived from the human BAC library RRC1-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (<http://inforesgen.com>). BAC end search page: http://www.tlig.org/cdb/hunguen/bac_end_search/bac_end_search.html. Class: BAC ends.

Query Match	4.0%	Score 36;	DB 12;	Length 614;	
Best Local Similarity	70.6%	Pred. No. 34;			
Matches 48; Conservative	0;	Mismatches 20;	Totals 6;	Cases 0	

QY	502	cgcgca	509
Db	172	CGGGAA	165

RESULT	19
LOCUS	BG107224
DEFINITION	BG107224 686 bp mRNA linear EST 30-JAN-2001 602290957F1 NIH_MGC_85 Homo sapiens CDNA clone IMAGE:4385583 5', mRNA sequence.

ACCESSION	BF107224
VERSION	BF107224.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

Query Match	4.0%;	Score 36;	DB 10;	Length 686;
Best Local Similarity	46.4%;	Pred. NO. 36;		
Matches 117; Conservative	0;	Mismatches 135;	Indels 0;	Gaps 0

224 GCCGCCCGGCCACATACAGCGAGCGGTGGCCGACCGGAGGACGACCCCAACTTTTTC 283

284 AAGATGGTGAAGGCTTCTTGATCGGGCGCCAGCATCGTGAGGACACACCTGCTGGAG 343

Db 344 GACCTGAGGACCCGGGAGAGCGAGGACGAGACGGAACGGGAACCGGTGCGCGCATCTGCGG 403

QY	550	atcatcaagcc	561
Db	404	ATCATCAAGCC	415

RESULT	20
LOCUS	BM461835
DEFINITION	BM461835 AGENCECORT 6A18362 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5533888
ACCESSION	BM461835
VERSION	BM461835.1
KEYWORDS	GI:18510875
SOURCE	EST.
	human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 970)
 NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12219 row: h column: 17
 High quality sequence stop: 506.
 Location/Qualifiers
 1..970
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:553388"
 /clone_lib="NIH-MGC-71"
 /tissue_type="leiomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1; NotI;
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.1 kb."
 BASE COUNT 181 a 307 c 302 g 179 t 1 others
 ORIGIN
 Query Match 4.0%; Score 36; DB 10; Length 970;
 Best Local Similarity 46.4%; Pred. No. 42; Mismatches 135; Indels 0; Gaps 0;
 Matches 117; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
 Oy 310 gcggtacacgctggaacatgtcagaagccttgacaacaacagaaggctgtatc 369
 Db 157 gcgttctggctggcgtggccggcgacagccgcccggcgacggcgctgcatg 216
 Oy 370 atcacgcgcacatgcagctacgattggcgagcgtatcacgcagcagctccg 429
 Db 217 gccggccggcgccactacagcagcgccggtggccgacgagcagcagccttcttc 276
 Oy 430 ttccgcctgacccgcatgtacaaacggcgaacaaatcaagcagatagacaatcatgca 489
 Db 277 aagatgtgtgagagccttcttgatgcggcgccagcagcagcagcagcagcagcagc 336
 Oy 490 gcgggacaggttcgcggaagaagaaacgcgcctaccagcatagcaggggtcaaaaca 549
 Db 337 gaccctgagagacccggagagagcagagcagaaacggagcagcagcagcagcagcagc 396
 Oy 550 atcatcaagcc 561
 Db 397 atcatcaagccc 408
 RESULT 21
 BM460646 1243 bp mRNA linear EST 05-FEB-2002
 LOCUS AGENCOURT_6421419 NIH-MGC_71 Homo sapiens CDNA clone IMAGE:5531991
 DEFINITION 5', mRNA sequence.
 ACCESSION BM460646
 VERSION BM460646.1 GI:18509686
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1243)
 NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12214 row: i column: 16
 High quality sequence stop: 439.
 Location/Qualifiers
 1..1243
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5531991"
 /clone_lib="NIH-MGC-71"
 /tissue_type="leiomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1; NotI;
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.1 kb."
 BASE COUNT 172 a 553 c 260 g 258 t
 ORIGIN
 Query Match 4.0%; Score 36; DB 10; Length 1243;
 Best Local Similarity 46.4%; Pred. No. 46; Mismatches 135; Indels 0; Gaps 0;
 Matches 117; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
 Oy 310 gcggtacacgctggaacatgtcagaagccttgacaacaacagaaggctgtatc 369
 Db 181 gcgttctggctggcgtggccggcgacagccgcccggcgacggcgctgcatg 240
 Oy 370 atcacgcgcacatgcagctacgattggcgagcgtatcacgcagcagcagctccg 429
 Db 241 gccggccggcgccactacagcagcgccggtggccgacgagcagcagcagcagcagcagc 300
 Oy 430 ttccgcctgacccgcatgtacaaacggcgaacaaatcaagcagatagacaatcatgca 489
 Db 301 aagatgtgtgagagccttcttgatgcggcgccagcagcagcagcagcagcagcagcagc 360
 Oy 490 gcgggacaggttcgcggaagaagaaacgcgcctaccagcatagcaggggtcaaaaca 549
 Db 361 gaccctgagagacccggagagcagagcagaaacggagcagcagcagcagcagcagcagc 420
 Oy 550 atcatcaagcc 561
 Db 421 atcatcaagccc 432
 RESULT 22
 BM466205 1247 bp mRNA linear EST 05-FEB-2002
 LOCUS AGENCOURT_6457149 NIH-MGC_92 Homo sapiens CDNA clone IMAGE:5576950
 DEFINITION 5', mRNA sequence.
 ACCESSION BM466205
 VERSION BM466205.1 GI:18515247
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1247)
 NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

QY 397 ttggcgagcgtacacagcagcagcttcggt 431
 Db 461 CGGACTACCTCTTCATCAGGATCTTGATTT 495

RESULT 27

CNS00CZP/C

LOCUS

CNS00CZP 914 bp DNA linear GSS 04-JUN-1999

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC # BACR26P05 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

AL059740.1 GI:4947405

KEYWORDS

GSS.

SOURCE

fruit fly.

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 914)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage; BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

COMMENT

- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see: http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamonos in Peter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2: cn bw sp. the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1..914
Location/Qualifiers
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR26P05"
/note="end : T7"

BASE COUNT

146 a 121 c 113 g 173 t 361 others

Query Match

4.0%; Score 35.8; DB 12; Length 914;
Best Local Similarity 18.4%; Pred. No. 46;

Matches

37; Conservative 92; Mismatches 72; Indels 0; Gaps 0;

QY 459

gaaatcaagcgtatagacaatcatcagcagcgagcaggttcgcgcaagaagaaac 518

Db 870

VVAATAAS 811

QY 519

cgcgcctaccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 578

Db 810

SSAS 751

QY 579

aacatcgtctcgtccgcagcagcagcagcagcagcagcagcagcagcagcagc 638

Db 750

SASMSAS 691

QY 639

ggaattcttcgcgaacatcgc 659

Db 690

GSTSAGMSVSCSSSACVCMSC 670

RESULT 28

CNS0166N/C

LOCUS

CNS0166N 1201 bp DNA linear GSS 26-JUN-1999

DEFINITION

Drosophila melanogaster genome survey sequence T7 end of BAC BACN15A22 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION

AL106361.1 GI:5621558

KEYWORDS

GSS.

SOURCE

fruit fly.

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 1201)

AUTHORS

Genoscope.

TITLE

Direct Submission

JOURNAL

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage; BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

COMMENT

- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CERN (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pGEM11.

FEATURES

source

1..1201
Location/Qualifiers
/organism="Drosophila melanogaster"
/plasmid="pGEM11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN15A22"
/note="end : T7"

BASE COUNT

146 a 231 c 260 g 313 t 251 others

Query Match

4.0%; Score 35.8; DB 12; Length 1201;
Best Local Similarity 25.4%; Pred. No. 52;

Matches

46; Conservative 65; Mismatches 70; Indels 0; Gaps 0;

QY 400

ggcgagcgtacacagcagcagcagcagcagcagcagcagcagcagcagcagc 459

Db 1127

GRRGMAAGVGMGVRCCRSASAGARACAVMACRCSSAMAAACAGARVAACRAMGAMM 1068

QY 460

aaatcaagcgtatagacaatcatcagcagcgagcaggttcgcgcaagaagaaac 519

Db 1067

AMAAAMMARACMGSMGSMGSMGSMGSMGSMGSMGSMGSMGSMGSMGSMGSM 1008

QY 520

gagcgtaccagcagcagcagcagcagcagcagcagcagcagcagcagcagc 579

Db 1007

KCGCGGACACGAGVMAAGSVMAACGSCRCVMGCMGCGVGVVVMVMAAAA 948

QY 580

a 580

Db 947

A 947

RESULT 29

BE965323

LOCUS

BE965323 1990 bp mRNA linear EST 14-DEC-2000

DEFINITION

601659233R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:385593 3', mRNA sequence.

ACCESSION

BE965323.2 GI:11769567

KEYWORDS

EST.

SOURCE

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

BASE COUNT	ORIGIN
100 a	61 c
64 g	101 t
4 others	

Query Match	3.9%	Score 35.4	DB 9	Length 330
Best Local Similarity	52.3%	Pred No. 39		
Matches 78	Conservative 0	Mismatches 71	Indels 0	Gaps 0
QY 596	accacgctccctccctcccaagaagcgcgggaaagcgctatggttgatcttcgcgcaac	655		
Db 201	ATCTCTTCCCTTCCCCCCCCAGTAAGCGTGGAGAGAGCGCTCTGGCAACTTCTTAATGCAAG	142		
QY 656	ctgcctatcacagcagcgcgcgcgcaaatctgcgcacgctcaagaagcgctgaaaacctgt	715		
Db 141	CAATGGTTAATTAATTTGTGAGCGCAGCTTTTAAGAGCGTTCAAGTAGGAATTAAGTCTG	82		
QY 716	ttcttcgcgcgagaagcgcctgcctgcgcgga	744		
Db 81	ATTATTATTAAGCAAAATGGCTGTTGGGGGA	53		

RESULT 33	BF622032	695 bp	mrna	linear	EST 17-OCT-2001
LOCUS	BF622032				
DEFINITION	BF622032				
	HYCNMA0001J08f Hordeum vulgare seedling shoot EST library				
	HYCNMA0001 (Cold stress) Hordeum vulgare cDNA clone HYCNMA0001J08f,				
	mrna sequence.				

DEFINITION	Brz202032 HVSMEAD0001J08f Hordeum vulgare seedling shoot EST library HYCDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMA0001J08f.
ACCESSION	B622032
VERSION	BF622032
KEYWORDS	EST.
SOURCE	BF622032.2 GI:13079666
ORGANISM	barley. Hordeum vulgare
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; 1 Triticeae; Hordeum. 1 (bases 1 to 695)
AUTHORS	Wing, R., Close, T.J., Kleinbofs, A., Wise, R., Begum, D., Frisch, D., Yu, ' Y., Henry, D.D., Palmer, M., Rambo, T., Slimmons, J., Oates, R., Chol, D.W., , Fenton, R.D., and Main, D. Development of a genetically and physically anchored EST resource for barley genomics: Morex cold-stressed seedling shoot cDNA library
TITLE	Unpublished (2001)
JOURNAL	On Dec 18, 2000 this sequence version replaced gi:11885766.
COMMENT	Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Total hg bases = 188 Seq primer: ATTATACCTCACTAAAGG High quality sequence stop: 669. Location/Qualifiers
FEATURES	1..695
Source	/organism="Hordeum vulgare" /cultivar="Morex" /db_xref="taxon:4513" /clone="HVSMEAD0001J08f" /clone_1lb="Hordeum vulgare seedling shoot EST library HYCDNA0001 (Cold stress)"

/tissue_type="Seedling shoot"

/lab_host="TJc121"

/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and ceftotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 50C for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give phagescript SK(-) cDNA phagemids. These steps were performed in the TJ Close Laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see

http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html)"

BASE COUNT
ORIGIN

130 a 229 c 230 g 105 t 1 others

Query Match

Best Local Similarity 55.2%; Pred. No. 53;

Matches 69; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 333 gcacgagcttgagcaaacaggaagcgtctatcatcagccgacatcgagcagta 392

Db 90 GCTGGCGCCGACGACACGAGGCGCAGGTGCGCTGGAGGCGCGCATCC 149

QY 393 cgattggcgagcgtacatcagcagcagcttcgcttcgctgacgacatgtaaa 452

Db 150 GGCCATCTCGCATCATCTCCACGACGCGCTGCCATCGGTGGCTCCATGAGCAT 209

QY 453 accgc 457

Db 210 GGCGC 214

RESULT 34

BF079098 568 bp mRNA linear EST 18-OCT-2000

LOCUS 229628 MABC 2P1G Sus scrofa cDNA 5', mRNA sequence.

DEFINITION BF079098

VERSION BF079098.1 GI:10872928

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

FEATURES

SOURCE

Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCGTCACGACG
Plate: 45 row: J column: 3
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1..568
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_1lb="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT
ORIGIN

104 a 170 c 182 g 111 t 1 others

Query Match

Best Local Similarity 48.5%; Pred. No. 55;

Matches 97; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 164 cgcgcatcgtcgcaatctgctgcagcagcagcagcagcagcagcagcagcagc 223

Db 438 CCCACAGCGTCATGCGCTCCGTCAGCGCTCCGTCAGCGCTCCGTCAGCGCT 379

QY 224 ccgcttgcggaagcagcagcagcagcagcagcagcagcagcagcagcagc 283

Db 378 AAGTGTCTGCGCCGACACAAAGAGCGCGCTGCTGCTGCTGCTGCTGCTGCT 319

QY 284 cgaagacatagaaacatggtcacaagcagcagcagcagcagcagcagcagcagc 343

Db 318 ATGTCCACATGTAGGACATCTCTCGGCGATTCGCTCCACACCATGACCAT 259

QY 344 tggacacacagcagcagcagcagcagcagcagcagcagcagcagcagc 363

Db 258 TCGGGAGAGCGCATGCGCTG 239

RESULT 35

AL502466 700 bp mRNA linear EST 04-JAN-2001

LOCUS AL502466 Hordeum vulgare Barke roots Hordeum vulgare cDNA clone

DEFINITION HM07K20u 3', mRNA sequence.

VERSION AL502466

ACCESSION AL502466.1 GI:12028681

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Institute for Plant Genetics and Crop Plant Research

Corrensstr. 3, D-06466 Gatersleben, Germany

Email: michael@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de

Seq primer: M3uni primer for 3' end.

Location/Qualifiers

1..700

/organism="Hordeum vulgare"

/cultivar="Barke"

/db_xref="taxon:4513"

/clone_1lb="HM07K20u"

/tissue_type="roots"

Query Match 3.9%; Score 35; DB 10; Length 822;
Best Local Similarity 48.3%; Pred. No. 74;
Matches 98; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 122 ggtcggacacatctggcgtttacatttaagaagacggcgagcatcgtccacata 181
DB 255 GGATCATTTGGTGTGGACTTGAACCTTGAACCAAGTACAAAGTTCGGCTGCA 314
QY 182 tgcgtcagcagcgtatgcacccgaccccaaacggtcaaacgcttttcggaacg 241
DB 315 CAGACTTTGTAACCCAAAGGACCAAGCCAGGAGAGGCTGTCGAGATGA 374
QY 242 caaaggcgttgcgaacttgcggccgcttttcagaagaacggaagacataagaa 301
DB 375 CAACGGCGGAGTGCAGACAGCAGTGAAGTGTACGGGACATTCGACCCATGATTCG 434
QY 302 tttcgaagcgtacacagcgtcg 324
DB 435 CCTTCGATGCTTCACGATGG 457

RESULT 40
BM047100 894 bp mRNA linear EST 07-NOV-2001
LOCUS 603627433F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5455761 5',
DEFINITION mRNA sequence.
ACCESSION BM047100
VERSION BM047100.1 GI:16776367
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DPF

CNA Library Preparation: Ling Hong/Rubin Laboratory
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL.at:
http://image.lnl.gov
Plate: LNCMI953 row: a column: 10
High quality sequence stop: 555.

FEATURES

source

Location/Qualifiers
1. 894
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5455761"
/clone_id="NIH_MGC_40"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT 172 a 334 c 253 g 135 t
ORIGIN

Query Match 3.9%; Score 35; DB 10; Length 894;
Best Local Similarity 63.9%; Pred. No. 77;
Matches 53; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 531 catcaagggtcaacaacatcatcaagccctgcgttcgagcaagacatcgtctc 590
DB 472 CAACACAGCTGTGCTCAACATCTTCCCAAGCGAGGTCCTCGGCTCGCAACCATCATCA 531
QY 591 gccgcagcagctccctccctc 613
DB 532 GGCATCTACGTCCACTACCTC 554

RESULT 41
AV869097 516 bp mRNA linear EST 08-NOV-2001
LOCUS AV869097/c
DEFINITION AV869097 Nori Satoh unpublished cDNA library, egg cDNA
ACCESSION AV869097
VERSION AV869097
KEYWORDS AV869097.1 GI:16856621
SOURCE EST.
ORGANISM Clona intestinalis.
Clona intestinalis

REFERENCE Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
AUTHORS phlebobranchia; Clonidae; Clona.
TITLE 1 (bases 1 to 516)
JOURNAL Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
COMMENT Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@acidian.zool.kyoto-u.ac.jp.

FEATURES

source

Location/Qualifiers
1. 516
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="rcieg35n07"
/clone_id="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
/dev_stage="egg"
BASE COUNT 63 a 137 c 135 g 181 t
ORIGIN

Query Match 3.9%; Score 34.8; DB 9; Length 516;
Best Local Similarity 52.0%; Pred. No. 69;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 412 atcagcagcagcttcggtccgctgacgcgcatgtacaacggcggaatcaagcg 471
DB 170 ACCACCGGAGAGGGCGCGGCCCAAGAGCGGCCCAAGTCGACAAAGAGACCGCC 111
QY 472 atgacaaaatcatcagcagcgaggttcgagcaagaagaacggcgctaccagc 531
DB 110 ACCAAACCAAGAAACCGCGAGGAGGAAACGCAAGTAAACCAAGCGCGCTCAAG 51
QY 532 atcagaggtcaacaacatcatcaagcc 561
DB 50 AACACAGCGCTCAAGAGCACTTAAGGC 21

RESULT 42
AL514205 565 bp mRNA linear EST 13-FEB-2001
LOCUS AL514205 LTI_NFL006.PL2 Homo sapiens cDNA clone Cl0BB006ZG12 3
DEFINITION prime, mRNA sequence.
ACCESSION AL514205
VERSION AL514205.1 GI:12777699
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE	1 (bases 1 to 565)
AUTHORS	Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage

BASE COUNT	171 a	25 c	135 g	143 t	91 others
ORIGIN					

[illegible]

BASE COUNT	129 a	284 c	278 g	144 t	5 others
ORIGIN					
Query Match	3.9%	Score 34.8;	DB 9;	Length 840;	
Best Local Similarity	52.1%;	Pred. No. 85;			
Matches	75;	Conservative	1;	Mismatches 68;	Indels 0;
				Gaps	0.

BASE COUNT	129 a	284 c	278 g	144 t	5 others
ORIGIN					

[illegible]

